

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 20:42:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046534.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR2046534 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046534_1.fastq.gz SRR2046534_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 20:42:27 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046534.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,777,684
Mapped reads	9,591,304 / 98.09%
Unmapped reads	186,380 / 1.91%
Mapped paired reads	9,591,304 / 98.09%
Mapped reads, first in pair	4,871,441 / 49.82%
Mapped reads, second in pair	4,719,863 / 48.27%
Mapped reads, both in pair	9,425,136 / 96.39%
Mapped reads, singletons	166,168 / 1.7%
Secondary alignments	0
Supplementary alignments	57,587 / 0.59%
Read min/max/mean length	30 / 100 / 100.24
Duplicated reads (estimated)	6,937,707 / 70.95%
Duplication rate	35.56%
Clipped reads	2,360,416 / 24.14%

2.2. ACGT Content

Number/percentage of A's	272,792,028 / 29.73%
Number/percentage of C's	186,961,762 / 20.37%
Number/percentage of T's	270,613,619 / 29.49%
Number/percentage of G's	187,180,801 / 20.4%
Number/percentage of N's	83,369 / 0.01%

GC Percentage	40.77%
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2.3. Coverage

Mean	0.2965
Standard Deviation	26.8226

2.4. Mapping Quality

Mean Mapping Quality	51.93
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2.5. Insert size

Mean	28,959.66
Standard Deviation	1,680,836.21
P25/Median/P75	101 / 126 / 155

2.6. Mismatches and indels

General error rate	0.45%
Mismatches	3,946,271
Insertions	79,421
Mapped reads with at least one insertion	0.81%
Deletions	94,244
Mapped reads with at least one deletion	0.95%
Homopolymer indels	47.14%

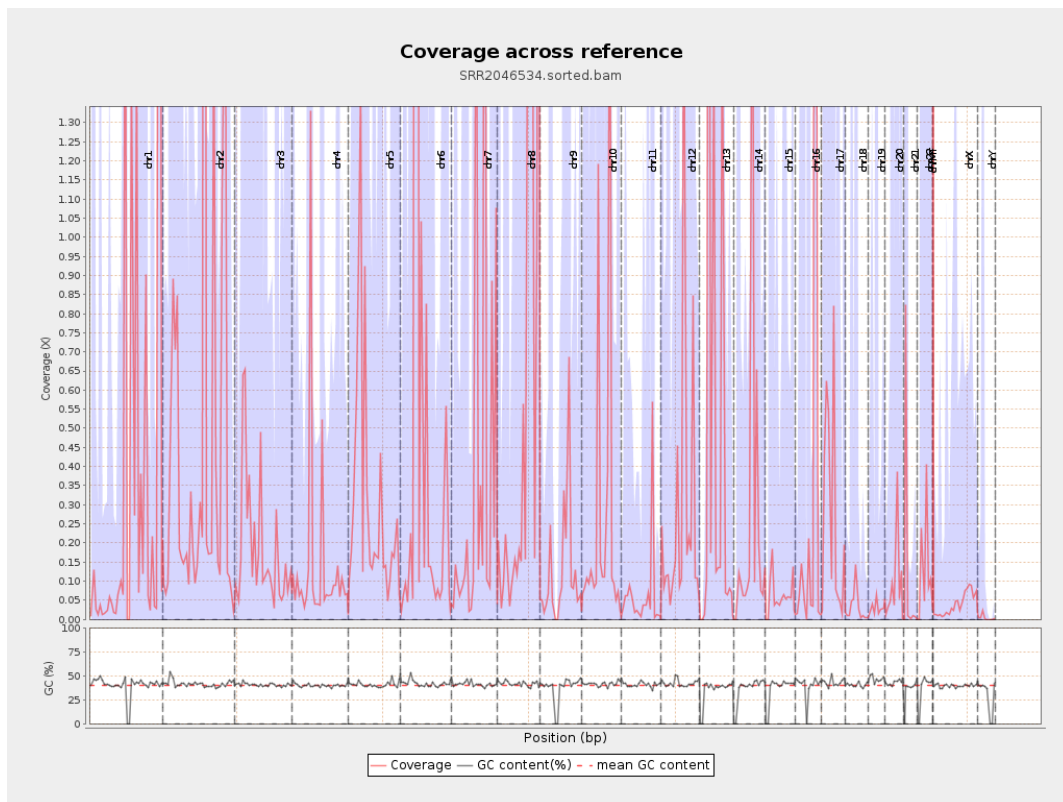
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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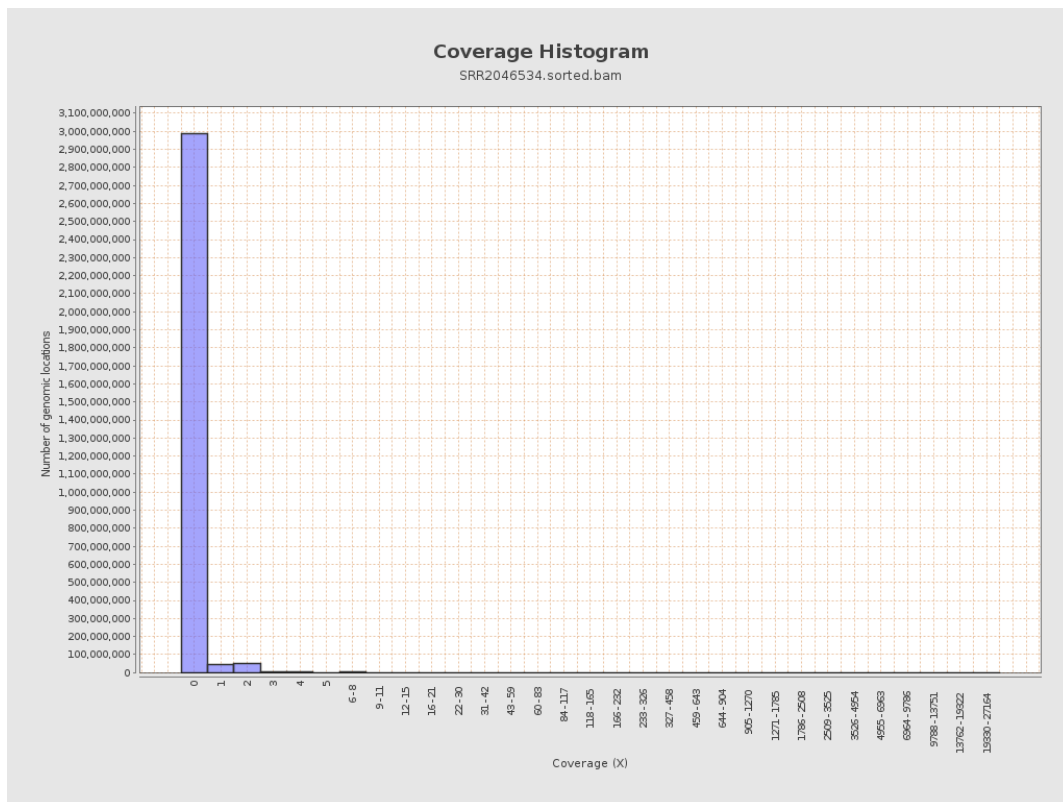
		bases	coverage	deviation
chr1	249250621	92488455	0.3711	28.0788
chr2	243199373	127582566	0.5246	31.9514
chr3	198022430	36745521	0.1856	9.8269
chr4	191154276	27231996	0.1425	13.3078
chr5	180915260	55949412	0.3093	15.2711
chr6	171115067	114047721	0.6665	65.184
chr7	159138663	67211091	0.4223	34.2238
chr8	146364022	121164894	0.8278	49.8405
chr9	141213431	17510399	0.124	11.0388
chr10	135534747	38083705	0.281	29.3471
chr11	135006516	8861966	0.0656	4.5676
chr12	133851895	37662882	0.2814	16.0165
chr13	115169878	54647387	0.4745	30.5065
chr14	107349540	28207456	0.2628	13.8495
chr15	102531392	6564382	0.064	3.8107
chr16	90354753	31551447	0.3492	28.7232
chr17	81195210	22083696	0.272	13.6029
chr18	78077248	2457850	0.0315	1.3865
chr19	59128983	1783394	0.0302	1.5606
chr20	63025520	6103580	0.0968	5.9375
chr21	48129895	6597540	0.1371	17.5222
chr22	51304566	6875677	0.134	7.2907
chrMT	16571	67582	4.0783	2.9827
chrX	155270560	6118451	0.0394	0.697

chrY	59373566	284130	0.0048	0.8733
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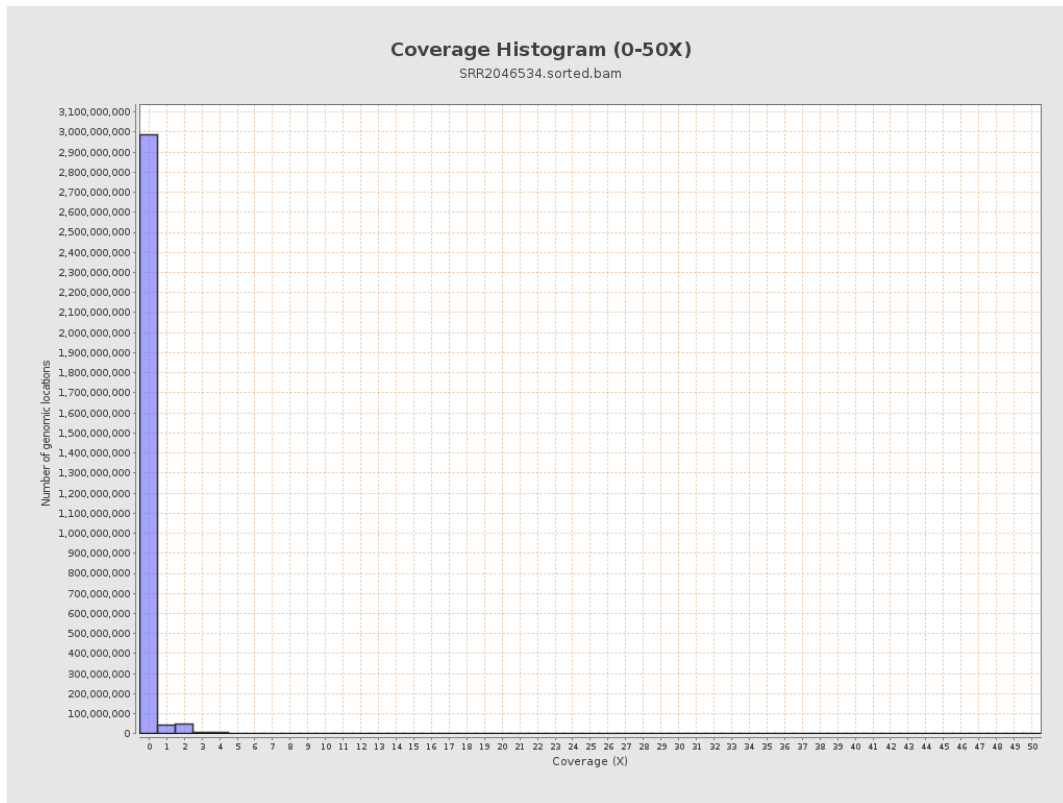
3. Results : Coverage across reference



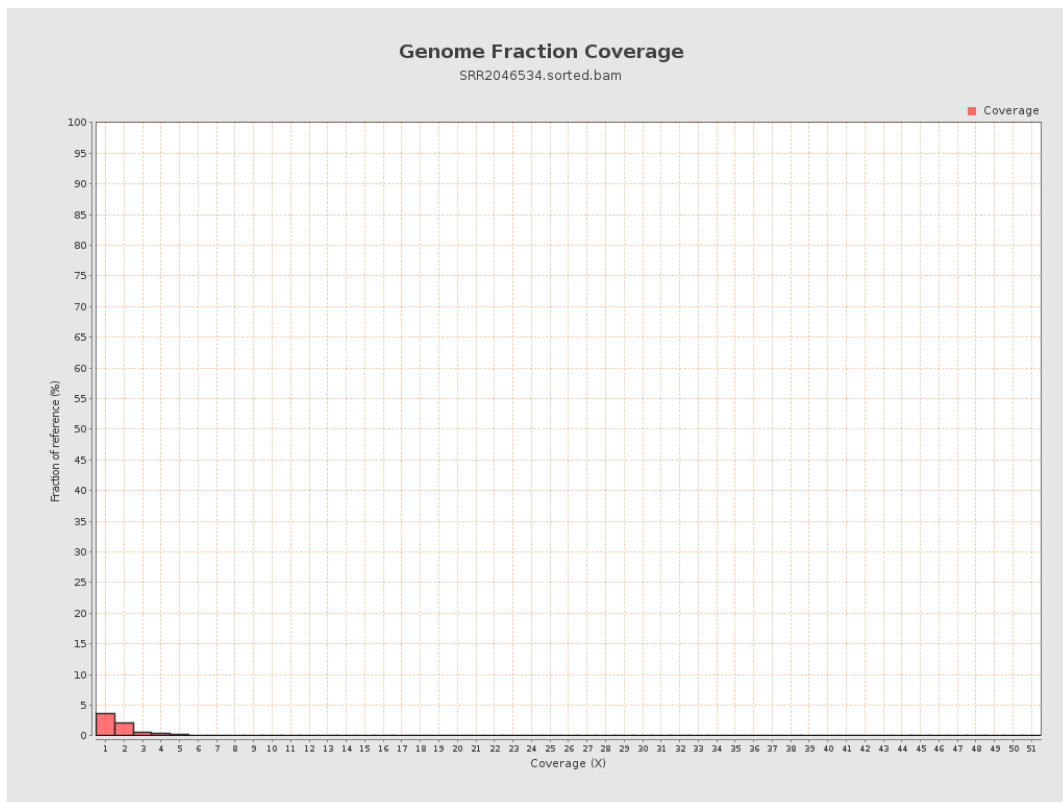
4. Results : Coverage Histogram



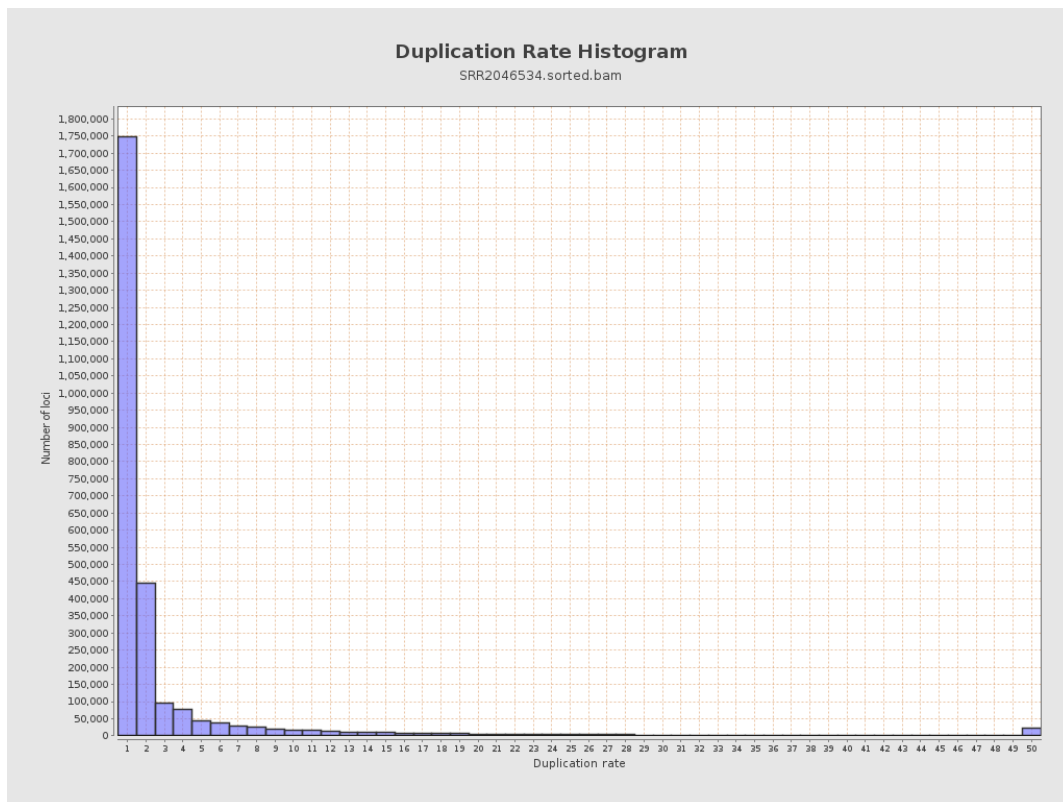
5. Results : Coverage Histogram (0-50X)



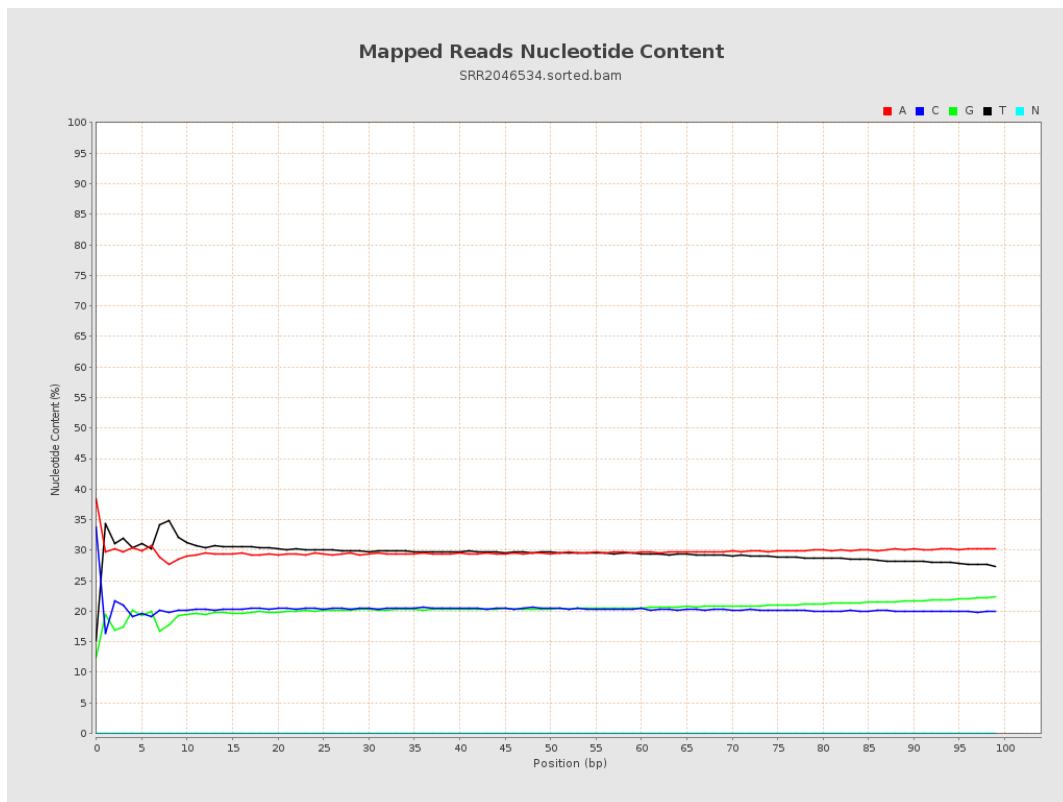
6. Results : Genome Fraction Coverage



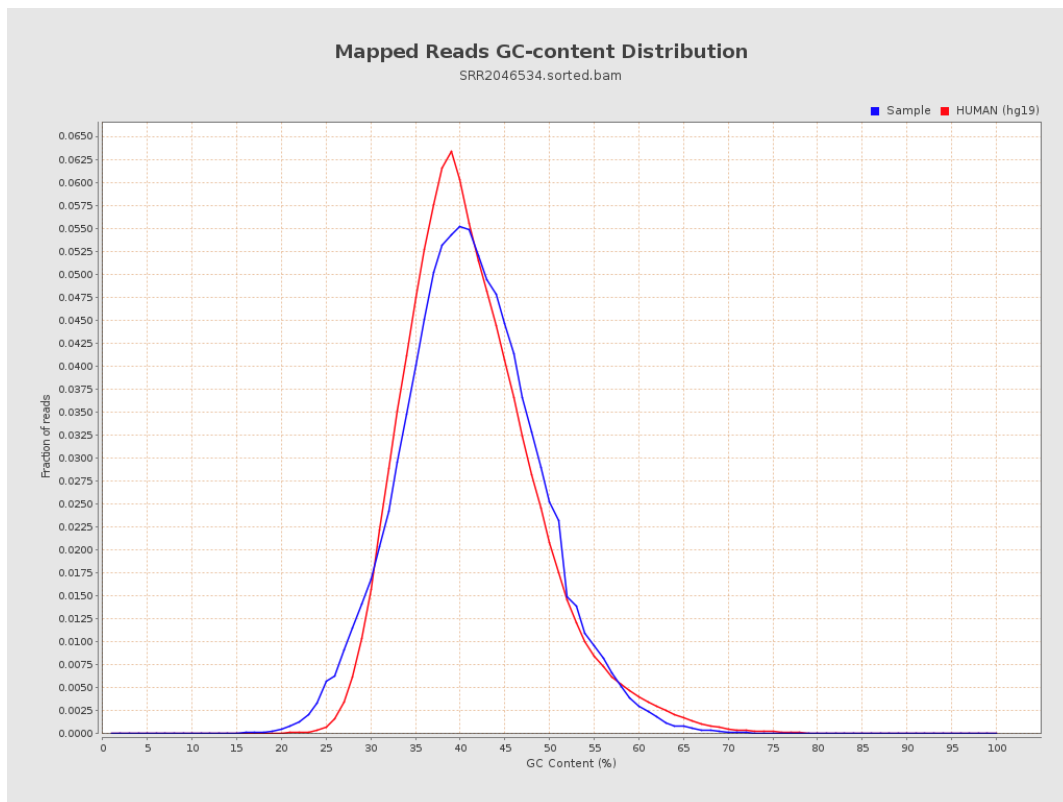
7. Results : Duplication Rate Histogram



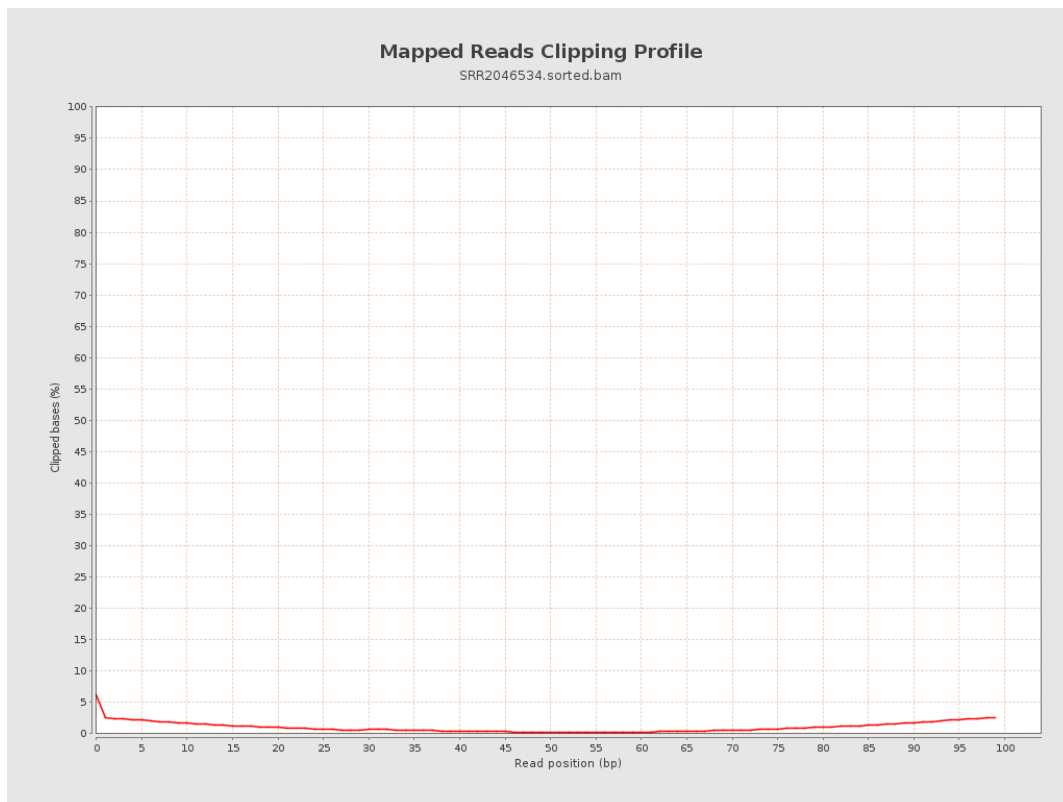
8. Results : Mapped Reads Nucleotide Content



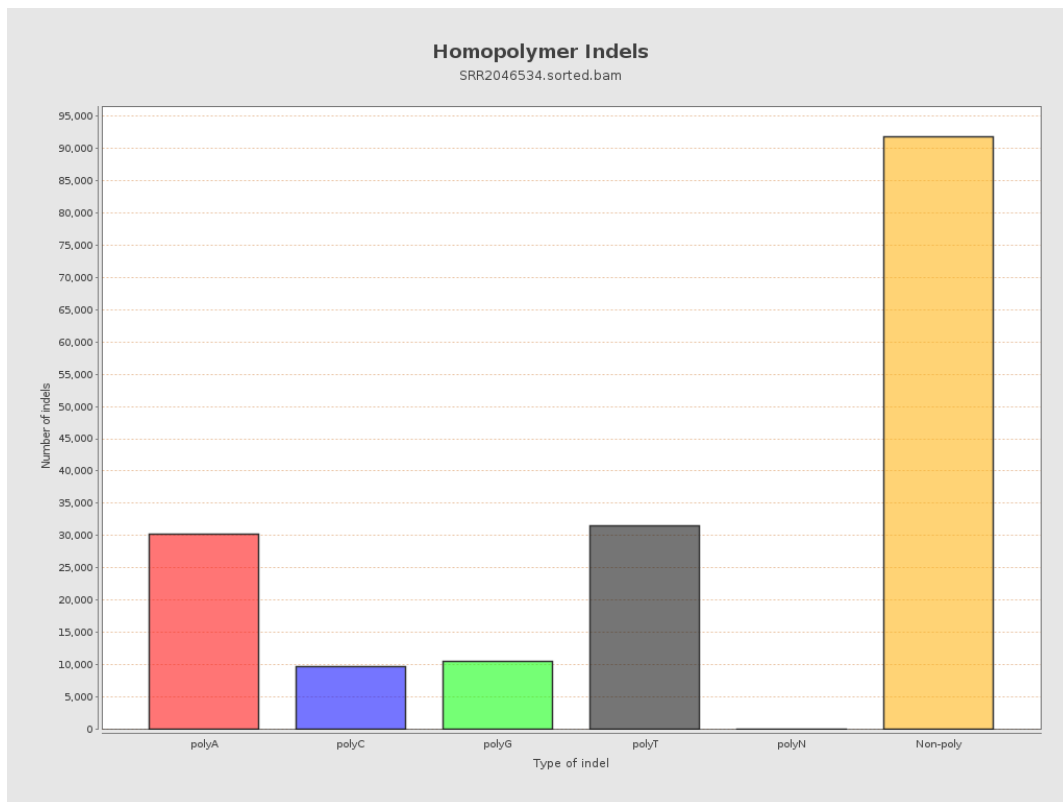
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



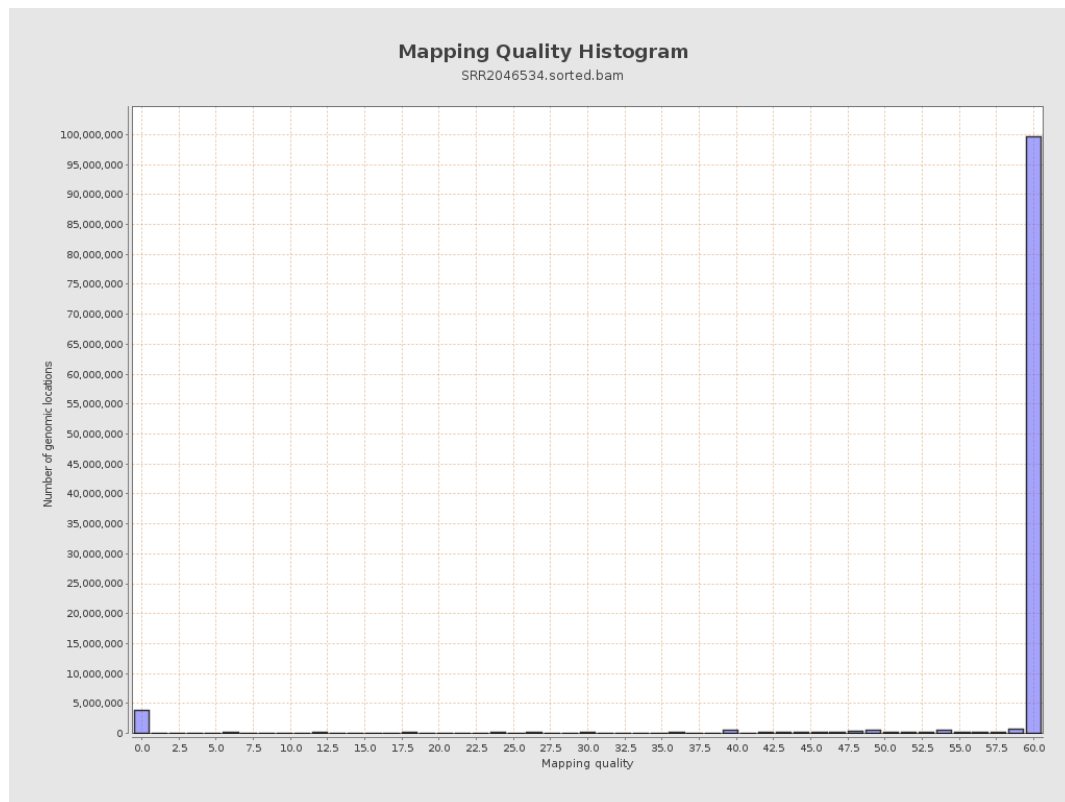
11. Results : Homopolymer Indels



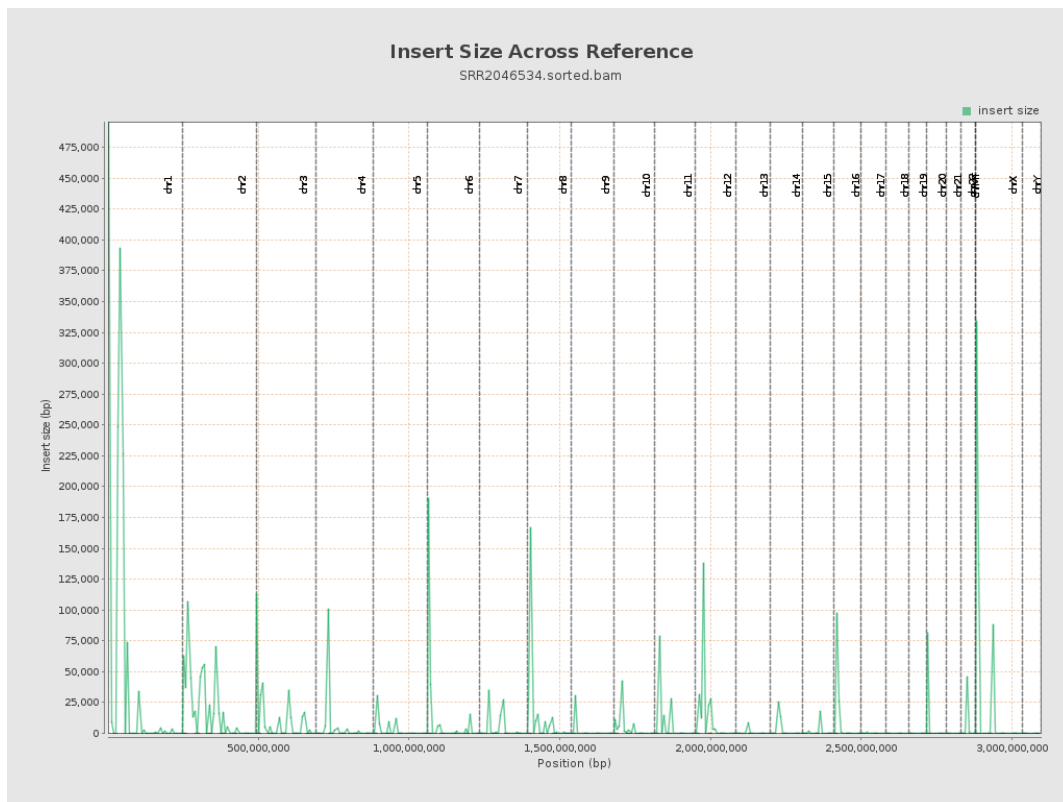
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

